

SEQUENCE LISTING

<110> Reed, John C.

<120> Plant Cytoprotective Genes and Methods
of Using Same

<130> P-LJ 4868

<150> US 09/661,014

<151> 2000-09-13

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 617

<212> DNA

<213> Lycopersicon esculentum

<220>

<221> CDS

<222> (103)...(594)

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cggtgcgtgg ctctgttgata ataccaagcg agaggagata ag atg ccg gaa cat 114
Met Pro Glu His
1

cct gct gca gac tca tca gcc acc gac aac acc gtc acc gtc aag cgt 162
Pro Ala Ala Asp Ser Ser Ala Thr Asp Asn Thr Val Thr Val Lys Arg
5 10 15 20

tat gcc cct ccc aat cag cgg aat cgt tca ctc ggc agg cga aaa tct 210
Tyr Ala Pro Pro Asn Gln Arg Asn Arg Ser Leu Gly Arg Arg Lys Ser
25 30 35

gga gat cga ctt gaa aga gct agc agc tat gct agt gat gga gag aag 258
Gly Asp Arg Leu Glu Arg Ala Ser Ser Tyr Ala Ser Asp Gly Glu Lys
40 45 50

aac caa atg aga gca gct aag tct gta tct gat gct gga gtc aat cga 306
Asn Gln Met Arg Ala Ala Lys Ser Val Ser Asp Ala Gly Val Asn Arg
55 60 65

gta aat gat tat cct cca aca aag tta ata ccg cta caa gga tgt tgt 354
Val Asn Asp Tyr Pro Pro Thr Lys Leu Ile Pro Leu Gln Gly Cys Cys
70 75 80

aca agc gaa gct ttt cag cta cta aat gac cgc tgg gca gct gct ctg 402

Thr	Ser	Glu	Ala	Phe	Gln	Leu	Leu	Asn	Asp	Arg	Trp	Ala	Ala	Ala	Leu	
85					90					95					100	
aat	gct	cat	aat	aat	tta	tca	gaa	gat	tct	cgt	gaa	agg	cct	gta	atg	450
Asn	Ala	His	Asn	Asn	Leu	Ser	Glu	Asp	Ser	Arg	Glu	Arg	Pro	Val	Met	
			105					110					115			
tac	aca	aaa	aga	tca	cct	tgg	ggg	cat	cct	ttt	ctt	cca	cat	caa	ttg	498
Tyr	Thr	Lys	Arg	Ser	Pro	Trp	Gly	His	Pro	Phe	Leu	Pro	His	Gln	Leu	
			120					125					130			
atg	tca	caa	gca	gga	gct	gaa	tct	tct	act	ggc	cag	aag	gat	ttt	cta	546
Met	Ser	Gln	Ala	Gly	Ala	Glu	Ser	Ser	Thr	Gly	Gln	Lys	Asp	Phe	Leu	
			135					140				145				
agc	aaa	ctt	cag	atg	gct	atg	ctc	aat	aca	cat	gtc	aat	ttc	gat	gcc	594
Ser	Lys	Leu	Gln	Met	Ala	Met	Leu	Asn	Thr	His	Val	Asn	Phe	Asp	Ala	
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taa atg ctat ccat ca agtg gtc 617

<210> 2
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 <212> PRT
 <213> Lycopersicon esculentum

<400> 2

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			20					25					30			
Arg	Arg	Lys	Ser	Gly	Asp	Arg	Leu	Glu	Arg	Ala	Ser	Ser	Tyr	Ala	Ser	
			35				40					45				
Asp	Gly	Glu	Lys	Asn	Gln	Met	Arg	Ala	Ala	Lys	Ser	Val	Ser	Asp	Ala	
			50			55					60					
Gly	Val	Asn	Arg	Val	Asn	Asp	Tyr	Pro	Pro	Thr	Lys	Leu	Ile	Pro	Leu	
65				70						75				80		
Gln	Gly	Cys	Cys	Thr	Ser	Glu	Ala	Phe	Gln	Leu	Leu	Asn	Asp	Arg	Trp	
			85					90					95			
Ala	Ala	Ala	Leu	Asn	Ala	His	Asn	Asn	Leu	Ser	Glu	Asp	Ser	Arg	Glu	
			100					105					110			
Arg	Pro	Val	Met	Tyr	Thr	Lys	Arg	Ser	Pro	Trp	Gly	His	Pro	Phe	Leu	
			115				120					125				
Pro	His	Gln	Leu	Met	Ser	Gln	Ala	Gly	Ala	Glu	Ser	Ser	Thr	Gly	Gln	
			130			135					140					
Lys	Asp	Phe	Leu	Ser	Lys	Leu	Gln	Met	Ala	Met	Leu	Asn	Thr	His	Val	
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<212> DNA
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<222> (87)...(830)

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actcgaagaa gaagaagaag agaaca atg gaa ggt ttc aca tcg ttc ttc gac 113
Met Glu Gly Phe Thr Ser Phe Phe Asp
1 5

tcg caa tct gcc tct cgc aac cgc tgg agt tat gat tct ctc aaa aac 161
Ser Gln Ser Ala Ser Arg Asn Arg Trp Ser Tyr Asp Ser Leu Lys Asn
10 15 20 25

ttc cgc cag atc tca cct ctc gtt caa act cat ctc aag cag gtg tac 209
Phe Arg Gln Ile Ser Pro Leu Val Gln Thr His Leu Lys Gln Val Tyr
30 35 40

ctt acg cta tgc tgt gct tta gtg gca tcg gct gct ggg gct tac ctt 257
Leu Thr Leu Cys Cys Ala Leu Val Ala Ser Ala Ala Gly Ala Tyr Leu
45 50 55

cac att cta tgg aat atc ggt ggc ctc ctc aca aca atg gct tgc atg 305
His Ile Leu Trp Asn Ile Gly Gly Leu Leu Thr Thr Met Ala Cys Met
60 65 70

gga agc atg gtg tgg ctt ctc tca gct cct cct tat caa gag caa aaa 353
Gly Ser Met Val Trp Leu Leu Ser Ala Pro Pro Tyr Gln Glu Gln Lys
75 80 85

agg gtg gct ctt ctg atg gca gct gca ctt ttt gaa ggc gcc tct att 401
Arg Val Ala Leu Leu Met Ala Ala Ala Leu Phe Glu Gly Ala Ser Ile
90 95 100 105

ggt cct ctg att gag ctg ggc att aac ttc gat cca agc att gtg ttt 449
Gly Pro Leu Ile Glu Leu Gly Ile Asn Phe Asp Pro Ser Ile Val Phe
110 115 120

ggc gct ttt gta ggt tgt gct gtg gtt ttt ggt tgc ttc tca gct gct 497
Gly Ala Phe Val Gly Cys Ala Val Val Phe Gly Cys Phe Ser Ala Ala
125 130 135

gcc atg ttg gca agg cgc agg gag tac ttg tac ctc ggg ggc ctt ctt 545
Ala Met Leu Ala Arg Arg Arg Glu Tyr Leu Tyr Leu Gly Gly Leu Leu
140 145 150

tca tct ggc gtc tcc ctt ctc ttc tgg ttg cac ttt gca tcc tcc att 593
Ser Ser Gly Val Ser Leu Leu Phe Trp Leu His Phe Ala Ser Ser Ile
155 160 165

ttt ggt ggt tcc atg gct gtt ttc aag ttt gag ttg tat ttt gga ctc 641
Phe Gly Gly Ser Met Ala Val Phe Lys Phe Glu Leu Tyr Phe Gly Leu
170 175 180 185

ttg gtg ttt gtg ggc tac atc gtc ttt gac acc caa gaa att att gag 689
Leu Val Phe Val Gly Tyr Ile Val Phe Asp Thr Gln Glu Ile Ile Glu
190 195 200

aag gct cac ttg ggt gat atg gat tac gtt aag cat gca ttg acc ctt 737
Lys Ala His Leu Gly Asp Met Asp Tyr Val Lys His Ala Leu Thr Leu
205 210 215

ttc aca gat ttt ggc gct gtt ttt gtg cgg att ctg atc atc atg tta 785
Phe Thr Asp Phe Gly Ala Val Phe Val Arg Ile Leu Ile Ile Met Leu
220 225 230

aag aat gca tct gag aag gaa gag aag aag aag aag agg aga aac 830
Lys Asn Ala Ser Glu Lys Glu Glu Lys Lys Lys Lys Arg Arg Asn
235 240 245

tagatttgct tctcaacttg tggttttccan aactccttgt gttcacctga aacaagcatg 890
ttaatagttt gatacttgct tcaacttttagc ataggctgtg atgtaatgtc gtgtgacatg 950
ccattatggc tgtgtgattg agcatctagc ctttttatct tctaaagctt ttttcttaac 1010
attgataagg aaagttcctt gtga 1034

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<212> PRT

<213> Lycopersicon esculentum

<400> 4

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Val Gln Thr His Leu Lys Gln Val Tyr Leu Thr Leu Cys Cys Ala Leu
35 40 45
Val Ala Ser Ala Ala Gly Ala Tyr Leu His Ile Leu Trp Asn Ile Gly
50 55 60
Gly Leu Leu Thr Thr Met Ala Cys Met Gly Ser Met Val Trp Leu Leu
65 70 75 80
Ser Ala Pro Pro Tyr Gln Glu Gln Lys Arg Val Ala Leu Leu Met Ala
85 90 95
Ala Ala Leu Phe Glu Gly Ala Ser Ile Gly Pro Leu Ile Glu Leu Gly
100 105 110
Ile Asn Phe Asp Pro Ser Ile Val Phe Gly Ala Phe Val Gly Cys Ala
115 120 125
Val Val Phe Gly Cys Phe Ser Ala Ala Ala Met Leu Ala Arg Arg Arg
130 135 140

Glu Tyr Leu Tyr Leu Gly Gly Leu Leu Ser Ser Gly Val Ser Leu Leu
 145 150 155 160
 Phe Trp Leu His Phe Ala Ser Ser Ile Phe Gly Gly Ser Met Ala Val
 165 170 175
 Phe Lys Phe Glu Leu Tyr Phe Gly Leu Leu Val Phe Val Gly Tyr Ile
 180 185 190
 Val Phe Asp Thr Gln Glu Ile Ile Glu Lys Ala His Leu Gly Asp Met
 195 200 205
 Asp Tyr Val Lys His Ala Leu Thr Leu Phe Thr Asp Phe Gly Ala Val
 210 215 220
 Phe Val Arg Ile Leu Ile Ile Met Leu Lys Asn Ala Ser Glu Lys Glu
 225 230 235 240
 Glu Lys Lys Lys Lys Arg Arg Asn
 245

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 <213> Artificial Sequence

<220>
 <223> primer

<400> 5
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28

<210> 6
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 <212> DNA
 <213> Artificial Sequence

<220>
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43

<210> 7
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<220>
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28